



Figure S4 LOD score comparison of the Lasso method (color coded in blue) with the composite interval mapping (CIM) method (color coded in red) and interval mapping (IM) method (color coded in green) for the first four traits (YD, TP, GN and KGW). The three horizontal dotted lines are the genome-wide 0.05 Type I error LOD score test critical values drawn from 1000 permuted samples. Natural bins were used in the analysis and the number of bins is 1619. LOD scores for the Lasso method that have reached the upper limit of the y-axis have been truncated, i.e., the actual LOD scores for those bins are higher than this limit.